



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:25 PM GMT

PDB ID : 4LL1
Title : The structure of the TRX and TXNIP complex
Authors : Hwang, J.; Kim, M.H.
Deposited on : 2013-07-09
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

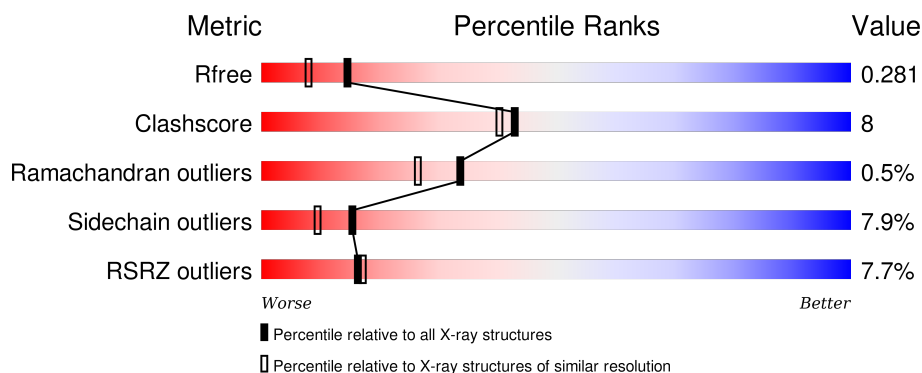
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	315	<div> <div>8%</div> <div> <div></div> <div>70%</div> <div>17%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	315	<div> <div>5%</div> <div> <div></div> <div>65%</div> <div>19%</div> <div>•</div> <div>11%</div> </div> </div>
2	B	105	<div> <div>16%</div> <div> <div></div> <div>76%</div> <div>23%</div> <div>•</div> </div> </div>
2	D	105	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>15%</div> <div>•</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6255 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Thioredoxin-interacting protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	S	0	0	0
			2177	1388	376	403	10			
1	C	280	Total	C	N	O	S	0	0	0
			2190	1391	381	408	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	120	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
A	170	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
A	205	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
A	267	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
C	120	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
C	170	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
C	205	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7
C	267	SER	CYS	ENGINEERED MUTATION	UNP Q9H3M7

- Molecule 2 is a protein called Thioredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	105	Total	C	N	O	S	0	0	0
			820	525	128	160	7			
2	D	105	Total	C	N	O	S	0	0	0
			820	525	128	160	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	35	ALA	CYS	ENGINEERED MUTATION	UNP P10599
D	35	ALA	CYS	ENGINEERED MUTATION	UNP P10599

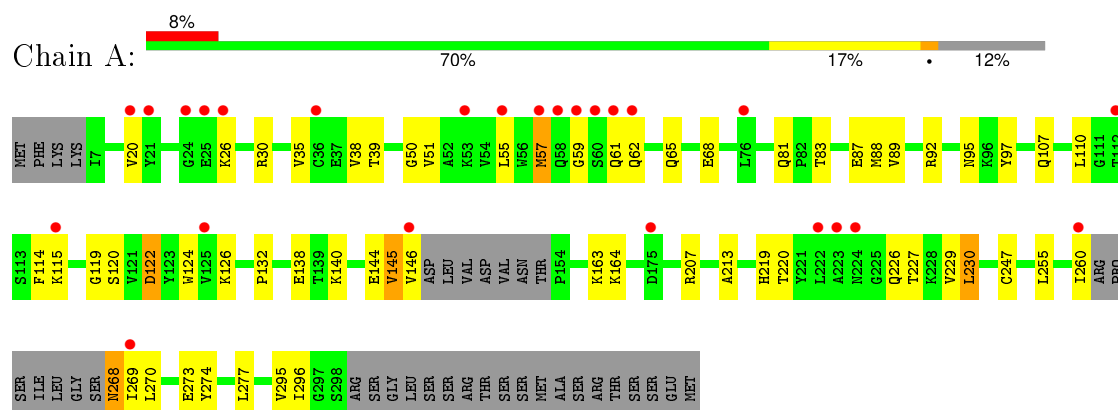
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	83	Total 83	O 83	0	0
3	B	18	Total 18	O 18	0	0
3	C	110	Total 110	O 110	0	0
3	D	37	Total 37	O 37	0	0

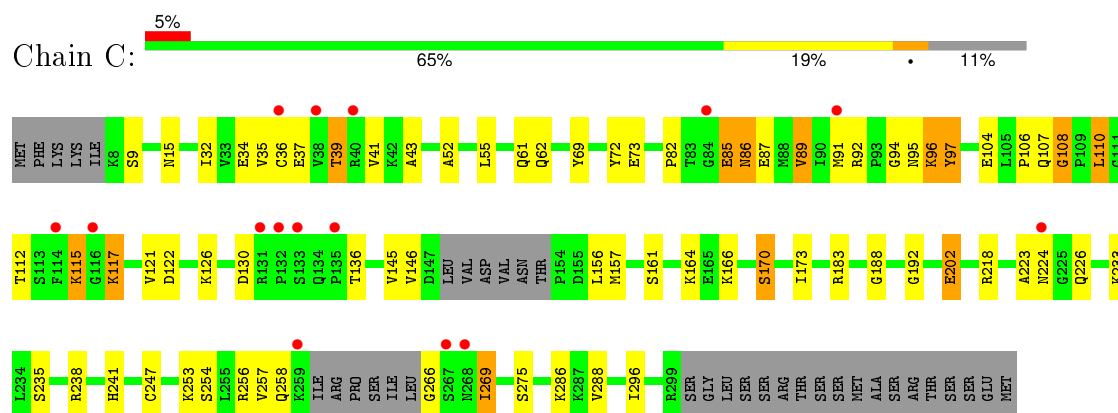
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

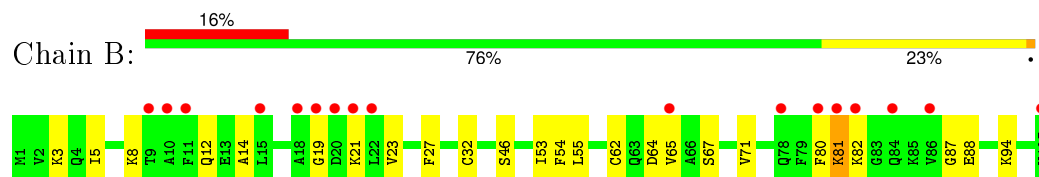
• Molecule 1: Thioredoxin-interacting protein



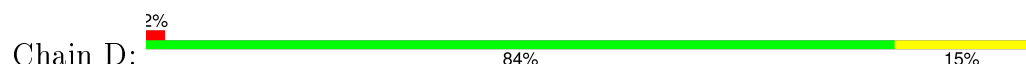
• Molecule 1: Thioredoxin-interacting protein

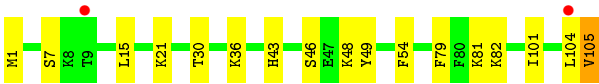


• Molecule 2: Thioredoxin



• Molecule 2: Thioredoxin





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.14Å 64.02Å 88.30Å 90.00° 91.28° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.4 (30.00-2.00) 96.4 (30.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.220 , 0.288 0.234 , 0.281	Depositor DCC
R_{free} test set	3077 reflections (5.53%)	DCC
Wilson B-factor (Å ²)	40.5	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.8	EDS
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 58910 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6255	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.66	0/2216	0.78	1/2986 (0.0%)
1	C	0.73	1/2229 (0.0%)	0.85	1/3002 (0.0%)
2	B	0.65	0/835	0.66	0/1121
2	D	0.73	1/835 (0.1%)	0.71	0/1121
All	All	0.69	2/6115 (0.0%)	0.78	2/8230 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	82	LYS	CE-NZ	5.58	1.63	1.49
1	C	97	TYR	C-O	5.44	1.33	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	94	GLY	CA-C-O	-5.33	111.01	120.60
1	A	230	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2177	0	2234	33	0
1	C	2190	0	2236	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	820	0	811	11	0
2	D	820	0	810	7	0
3	A	83	0	0	1	0
3	B	18	0	0	2	0
3	C	110	0	0	4	0
3	D	37	0	0	0	0
All	All	6255	0	6091	98	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (98) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:266:GLY:O	1:C:269:ILE:HG22	1.68	0.94
1:C:55:LEU:HG	1:C:62:GLN:HE21	1.32	0.92
1:C:34:GLU:OE2	1:C:96:LYS:HG3	1.77	0.84
1:C:73:GLU:HG2	3:C:417:HOH:O	1.80	0.80
1:C:156:LEU:HD23	1:C:157:MET:HE2	1.64	0.79
1:C:35:VAL:HG11	1:C:39:THR:HG21	1.66	0.77
1:A:35:VAL:HG21	1:A:39:THR:OG1	1.87	0.75
1:A:219:HIS:O	1:A:229:VAL:HA	1.89	0.73
1:C:170:SER:HB3	1:C:173:ILE:H	1.53	0.73
1:C:202:GLU:HG2	1:C:247:CYS:SG	2.30	0.72
1:C:35:VAL:HG11	1:C:39:THR:CG2	2.20	0.72
1:C:41:VAL:HB	1:C:89:VAL:HG13	1.73	0.71
1:A:230:LEU:HD12	1:C:85:GLU:HG3	1.77	0.67
2:B:62:CYS:HB3	2:B:65:VAL:HG12	1.76	0.67
1:C:55:LEU:CG	1:C:62:GLN:HE21	2.05	0.67
1:A:274:TYR:CG	1:A:296:ILE:HD13	2.29	0.67
1:C:69:TYR:O	1:C:106:PRO:HG3	1.95	0.67
1:A:20:VAL:HG22	1:A:144:GLU:HG2	1.76	0.67
1:C:156:LEU:HD23	1:C:157:MET:CE	2.25	0.66
1:C:32:ILE:HA	1:C:97:TYR:O	1.95	0.66
1:C:107:GLN:O	1:C:108:GLY:O	2.17	0.62
1:C:91:MET:HE2	1:C:97:TYR:CD2	2.36	0.61
2:B:94:LYS:HG3	3:B:210:HOH:O	2.00	0.60
1:C:115:LYS:CE	1:C:122:ASP:OD2	2.51	0.59
1:A:226:GLN:HE21	1:C:72:TYR:HD1	1.50	0.58
1:A:274:TYR:CB	1:A:296:ILE:HD13	2.35	0.56
2:B:5:ILE:HD11	2:B:55:LEU:HD22	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:LYS:NZ	1:C:286:LYS:O	2.39	0.55
2:B:81:LYS:NZ	3:B:201:HOH:O	2.26	0.54
2:D:81:LYS:NZ	2:D:104:LEU:O	2.40	0.53
1:C:112:THR:HG23	1:C:146:VAL:HA	1.91	0.53
1:C:192:GLY:N	1:C:257:VAL:O	2.34	0.53
1:C:55:LEU:CG	1:C:62:GLN:NE2	2.69	0.53
1:A:83:THR:O	1:C:233:LYS:HB2	2.09	0.53
2:B:23:VAL:CG1	2:B:80:PHE:HB2	2.39	0.53
1:C:156:LEU:CD2	1:C:157:MET:HE2	2.37	0.52
1:C:91:MET:CE	1:C:97:TYR:CD2	2.92	0.52
1:A:126:LYS:HD3	1:A:138:GLU:OE2	2.10	0.51
1:A:114:PHE:O	1:A:119:GLY:HA3	2.10	0.51
1:C:110:LEU:HD13	1:C:145:VAL:HG11	1.93	0.51
1:C:218:ARG:NH2	1:C:275:SER:OG	2.41	0.51
1:A:88:MET:SD	1:A:132:PRO:HG3	2.52	0.50
1:C:91:MET:HE2	1:C:97:TYR:CE2	2.47	0.50
1:A:273:GLU:HG2	3:A:455:HOH:O	2.11	0.50
1:A:83:THR:HB	1:C:233:LYS:HD2	1.93	0.49
2:D:79:PHE:HE2	2:D:101:ILE:HG13	1.78	0.49
1:C:161:SER:HB3	1:C:183:ARG:HG3	1.95	0.49
1:A:277:LEU:HD13	1:C:82:PRO:HB2	1.94	0.49
1:A:220:THR:HG23	1:A:227:THR:CG2	2.42	0.49
1:C:115:LYS:HE3	1:C:122:ASP:OD2	2.13	0.48
1:C:52:ALA:CB	1:C:121:VAL:HG22	2.44	0.48
2:D:101:ILE:O	2:D:105:VAL:HG22	2.13	0.48
1:A:65:GLN:OE1	1:A:295:VAL:HG13	2.13	0.48
1:C:37:GLU:O	1:C:39:THR:HG22	2.14	0.47
1:C:55:LEU:HG	1:C:62:GLN:NE2	2.12	0.47
2:D:46:SER:HA	2:D:54:PHE:CE1	2.50	0.47
2:B:19:GLY:H	2:B:21:LYS:HG2	1.80	0.47
1:C:223:ALA:O	1:C:224:ASN:C	2.54	0.46
1:A:247:CYS:CB	2:B:32:CYS:HG	2.24	0.46
1:C:238:ARG:HH12	1:C:241:HIS:CE1	2.34	0.46
1:A:57:MET:HA	1:A:61:GLN:O	2.15	0.46
1:C:115:LYS:HE2	1:C:122:ASP:OD2	2.16	0.46
1:A:35:VAL:HG21	1:A:39:THR:HG1	1.81	0.45
1:A:213:ALA:HA	1:A:277:LEU:O	2.17	0.45
1:A:220:THR:HG22	1:A:270:LEU:HD12	1.98	0.45
2:B:87:GLY:O	2:B:88:GLU:HB2	2.16	0.45
1:C:130:ASP:HA	1:C:136:THR:HG22	1.99	0.44
1:C:55:LEU:HD21	1:C:62:GLN:NE2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3:LYS:HE3	2:B:3:LYS:HB2	1.80	0.44
1:C:226:GLN:NE2	3:C:430:HOH:O	2.44	0.44
2:D:1:MET:SD	2:D:43:HIS:HE1	2.40	0.44
1:C:156:LEU:CD2	1:C:157:MET:CE	2.95	0.44
1:A:51:VAL:HG22	1:A:68:GLU:HG2	2.00	0.43
1:C:110:LEU:HD13	1:C:145:VAL:CG1	2.48	0.43
1:A:255:LEU:HD23	1:A:255:LEU:HA	1.80	0.43
1:A:124:TRP:CZ3	1:A:126:LYS:HG3	2.54	0.43
1:C:156:LEU:HD21	1:C:188:GLY:HA3	2.01	0.43
1:A:81:GLN:HG3	1:A:89:VAL:HG22	2.00	0.43
1:A:268:ASN:HD22	1:A:268:ASN:HA	1.60	0.42
1:C:55:LEU:HD21	1:C:62:GLN:HE22	1.84	0.42
1:C:43:ALA:HB3	1:C:130:ASP:HB2	2.02	0.42
1:A:126:LYS:HE3	1:A:140:LYS:HD2	2.02	0.42
1:A:50:GLY:HA2	1:A:122:ASP:O	2.19	0.42
1:A:269:ILE:HG13	1:A:269:ILE:O	2.18	0.42
1:A:110:LEU:HD13	1:A:145:VAL:HG22	2.02	0.41
1:C:86:ASN:O	1:C:87:GLU:C	2.57	0.41
1:C:15:ASN:OD1	3:C:497:HOH:O	2.22	0.41
1:C:257:VAL:HG13	1:C:296:ILE:HD13	2.03	0.41
1:A:20:VAL:HG22	1:A:144:GLU:CG	2.48	0.41
2:B:27:PHE:CG	2:B:71:VAL:HG21	2.55	0.41
2:B:46:SER:HA	2:B:54:PHE:CE1	2.56	0.41
1:C:85:GLU:H	1:C:85:GLU:HG2	1.47	0.41
1:C:170:SER:HB2	3:C:438:HOH:O	2.20	0.41
1:A:95:ASN:HB2	1:A:97:TYR:CE2	2.55	0.41
1:C:112:THR:O	1:C:121:VAL:HB	2.21	0.40
2:D:48:LYS:HD3	2:D:49:TYR:CE2	2.56	0.40
2:D:30:THR:O	2:D:36:LYS:HE2	2.20	0.40
1:A:38:VAL:HG22	1:A:92:ARG:HG2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	272/315 (86%)	259 (95%)	12 (4%)	1 (0%)	39	33
1	C	274/315 (87%)	262 (96%)	10 (4%)	2 (1%)	26	19
2	B	103/105 (98%)	96 (93%)	6 (6%)	1 (1%)	19	11
2	D	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
All	All	752/840 (90%)	716 (95%)	32 (4%)	4 (0%)	34	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	14	ALA
1	A	59	GLY
1	C	117	LYS
1	C	108	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	243/277 (88%)	226 (93%)	17 (7%)	19	12
1	C	244/277 (88%)	219 (90%)	25 (10%)	9	5
2	B	91/91 (100%)	84 (92%)	7 (8%)	16	10
2	D	91/91 (100%)	87 (96%)	4 (4%)	35	30
All	All	669/736 (91%)	616 (92%)	53 (8%)	15	9

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LYS
1	A	30	ARG
1	A	55	LEU
1	A	57	MET

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Mol	Chain	Res	Type
1	A	62	GLN
1	A	87	GLU
1	A	107	GLN
1	A	115	LYS
1	A	120	SER
1	A	122	ASP
1	A	145	VAL
1	A	146	VAL
1	A	163	LYS
1	A	164	LYS
1	A	207	ARG
1	A	260	ILE
1	A	268	ASN
2	B	8	LYS
2	B	12	GLN
2	B	53	ILE
2	B	64	ASP
2	B	67	SER
2	B	81	LYS
2	B	82	LYS
1	C	9	SER
1	C	36	CYS
1	C	39	THR
1	C	61	GLN
1	C	85	GLU
1	C	86	ASN
1	C	89	VAL
1	C	92	ARG
1	C	95	ASN
1	C	96	LYS
1	C	104	GLU
1	C	110	LEU
1	C	115	LYS
1	C	117	LYS
1	C	126	LYS
1	C	164	LYS
1	C	170	SER
1	C	202	GLU
1	C	235	SER
1	C	253	LYS
1	C	254	SER
1	C	256	ARG

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Mol	Chain	Res	Type
1	C	258	GLN
1	C	269	ILE
1	C	288	VAL
2	D	7	SER
2	D	15	LEU
2	D	21	LYS
2	D	105	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	219	HIS
1	A	224	ASN
1	A	268	ASN
2	B	102	ASN
1	C	62	GLN
1	C	142	ASN
1	C	241	HIS
1	C	258	GLN
2	D	43	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	278/315 (88%)	0.72	25 (8%)	12 12	33, 62, 110, 140	0
1	C	280/315 (88%)	0.28	15 (5%)	29 31	26, 46, 81, 96	0
2	B	105/105 (100%)	0.79	17 (16%)	3 3	23, 73, 171, 185	0
2	D	105/105 (100%)	0.02	2 (1%)	70 70	24, 54, 109, 131	0
All	All	768/840 (91%)	0.47	59 (7%)	16 17	23, 56, 116, 185	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	SER	7.4
1	C	133	SER	5.8
1	A	59	GLY	5.6
1	A	57	MET	5.3
1	C	267	SER	4.8
1	C	132	PRO	4.8
2	B	80	PHE	4.7
2	B	84	GLN	4.4
1	C	38	VAL	4.3
1	A	58	GLN	4.2
2	B	15	LEU	4.2
2	B	10	ALA	4.2
2	B	82	LYS	4.1
1	C	36	CYS	4.1
1	C	114	PHE	3.9
1	A	61	GLN	3.9
2	B	105	VAL	3.7
1	C	135	PRO	3.6
2	B	81	LYS	3.6
1	A	269	ILE	3.5
1	A	20	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	86	VAL	3.2
1	A	26	LYS	3.2
2	B	20	ASP	3.2
1	C	40	ARG	3.1
1	C	116	GLY	3.1
2	B	11	PHE	3.1
2	B	18	ALA	3.1
2	B	21	LYS	3.1
2	B	65	VAL	3.1
1	A	21	TYR	3.0
1	A	55	LEU	3.0
1	C	268	ASN	3.0
1	A	175	ASP	2.9
1	A	260	ILE	2.9
1	A	62	GLN	2.9
1	A	224	ASN	2.8
2	D	9	THR	2.8
1	A	76	LEU	2.7
1	A	53	LYS	2.7
1	A	25	GLU	2.6
1	C	224	ASN	2.6
1	A	222	LEU	2.5
1	A	112	THR	2.5
1	C	84	GLY	2.4
2	B	22	LEU	2.4
1	A	223	ALA	2.3
1	A	146	VAL	2.3
1	A	125	VAL	2.2
1	A	115	LYS	2.2
1	C	91	MET	2.2
2	B	19	GLY	2.2
1	A	24	GLY	2.2
1	C	131	ARG	2.1
2	B	9	THR	2.1
1	A	36	CYS	2.1
1	C	259	LYS	2.0
2	D	104	LEU	2.0
2	B	78	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.